

Figure 1A

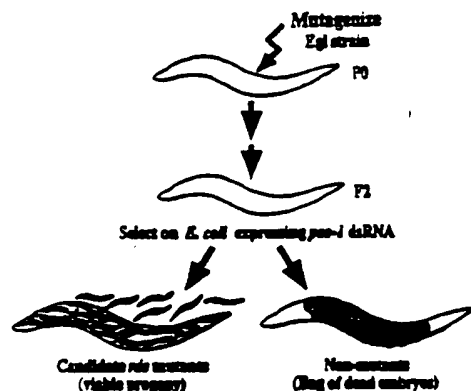


Figure B

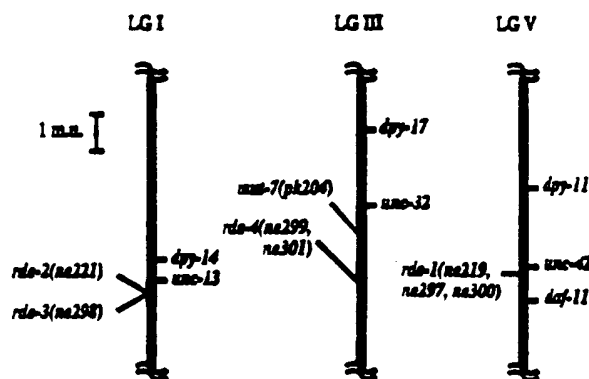


Figure 2

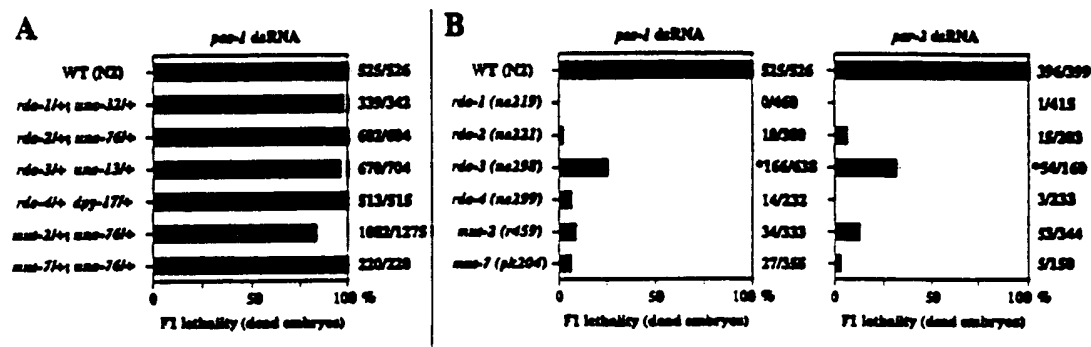
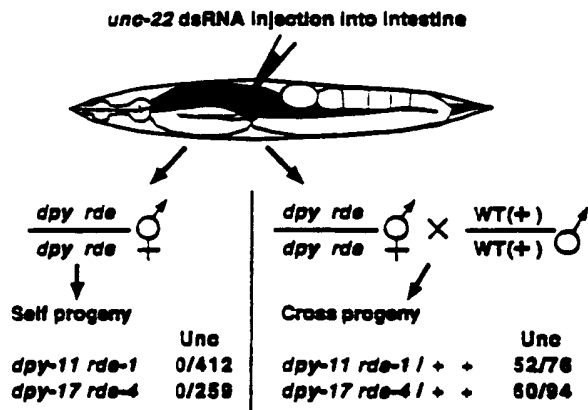
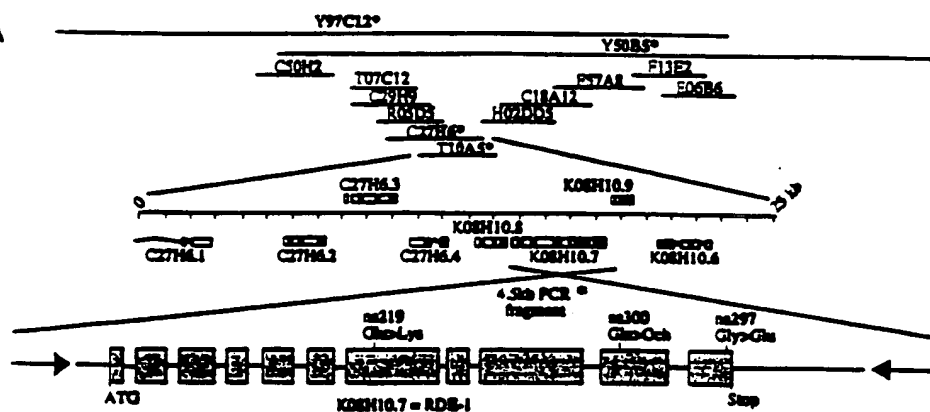


Figure 3



A



B

Line	Text	Page
100-1	103	1
P4877.1	128	1
0172C	77	1
SWELLB	126	1
SLing	189	1
100-1	107	1
P4877.1	119	1
0172C	166	1
SWELLB	199	1
SLing	164	1
100-1	110	1
P4877.1	400	1
0172C	120	1
SWELLB	172	1
SLing	108	1
100-1	114	1
P4877.1	484	1
0172C	100	1
SWELLB	484	1
SLing	196	1
100-1	114	1
P4877.1	501	1
0172C	192	1
SWELLB	543	1
SLing	408	1
100-1	104	1
P4877.1	410	1
0172C	440	1
SWELLB	420	1
SLing	523	1
100-1	104	1
P4877.1	728	1
0172C	320	1
SWELLB	691	1
SLing	621	1
100-1	700	1
P4877.1	792	1
0172C	483	1
SWELLB	779	1
SLing	687	1
100-1	670	1
P4877.1	668	1
0172C	679	1
SWELLB	683	1
SLing	766	1
100-1	660	1
P4877.1	636	1
0172C	747	1
SWELLB	631	1
SLing	627	1

figure -

0966992 101300

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Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital Status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	3000	1500	1000	6000
Health	0.5	0.5	0	1
Smoking	0.2	0.4	0	1
Drinking	0.1	0.3	0	1
Exercise	0.3	0.5	0	1
Stress	0.4	0.5	0	1
Sleep	0.5	0.5	0	1
Work	0.5	0.5	0	1
Family	0.5	0.5	0	1
Friends	0.5	0.5	0	1
Hobbies	0.5	0.5	0	1
Travel	0.5	0.5	0	1
Volunteering	0.5	0.5	0	1
Religion	0.5	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.5	0.5	0	1
Music	0.5	0.5	0	1
Gardening	0.5	0.5	0	1
Cooking	0.5	0.5	0	1
Reading	0.5	0.5	0	1
Writing	0.5	0.5	0	1
Learning	0.5	0.5	0	1
Teaching	0.5	0.5	0	1
Managing	0.5	0.5	0	1
Organizing	0.5	0.5	0	1
Planning	0.5	0.5	0	1
Decision Making	0.5	0.5	0	1
Problem Solving	0.5	0.5	0	1
Communication	0.5	0.5	0	1
Interpersonal Skills	0.5	0.5	0	1
Leadership	0.5	0.5	0	1
Teamwork	0.5	0.5	0	1
Conflict Resolution	0.5	0.5	0	1
Emotional Stability	0.5	0.5	0	1
Resilience	0.5	0.5	0	1
Adaptability	0.5	0.5	0	1
Flexibility	0.5	0.5	0	1
Openness	0.5	0.5	0	1
Conscientiousness	0.5	0.5	0	1
Agreeableness	0.5	0.5	0	1
Neuroticism	0.5	0.5	0	1
Extraversion	0.5	0.5	0	1
Introversion	0.5	0.5	0	1
Optimism	0.5	0.5	0	1
Pessimism	0.5	0.5	0	1
Self-Esteem	0.5	0.5	0	1
Self-Confidence	0.5	0.5	0	1
Self-Motivation	0.5	0.5	0	1
Self-Discipline	0.5	0.5	0	1
Self-Regulation	0.5	0.5	0	1
Self-Improvement	0.5	0.5	0	1
Self-Reflection	0.5	0.5	0	1
Self-Analysis	0.5	0.5	0	1
Self-Insight	0.5	0.5	0	1
Self-Knowledge	0.5	0.5	0	1
Self-Understanding	0.5	0.5	0	1
Self-Awareness	0.5	0.5	0	1
Self-Perception	0.5	0.5	0	1
Self-Image	0.5	0.5	0	1
Self-Concept	0.5	0.5	0	1
Self-Identity	0.5	0.5	0	1
Self-Expression	0.5	0.5	0	1
Self-Communication	0.5	0.5	0	1
Self-Interaction	0.5	0.5	0	1
Self-Relationship	0.5	0.5	0	1
Self-Connection	0.5	0.5	0	1
Self-Engagement	0.5	0.5	0	1
Self-Participation	0.5	0.5	0	1
Self-Involvement	0.5	0.5	0	1
Self-Commitment	0.5	0.5	0	1
Self-Dedication	0.5	0.5	0	1
Self-Sacrifice	0.5	0.5	0	1
Self-Service	0.5	0.5	0	1
Self-Help	0.5	0.5	0	1
Self-Reliance	0.5	0.5	0	1
Self-Dependence	0.5	0.5	0	1
Self-Sufficiency	0.5	0.5	0	1
Self-Independence	0.5	0.5	0	1
Self-Freedom	0.5	0.5	0	1
Self-Choice	0.5	0.5	0	1
Self-Action	0.5			

1/1 31/1:  
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Met ser ser asn pro glu leu glu lys gly pro tyr arg his ser leu asp pro glu

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met lys trp leu ala arg pro thr gly lys cys asp gly lys phe tyr glu lys lys val

121/41 151/51  
CTT CTT TTG GTA AAT TGG TTC AAG TTC TCC AGC AAA ATT TAC GAT CGG GAA TAC TAC GAG  
leu leu leu val asn trp phe lys phe ser ser lys ile tyr asp arg glu tyr tyr glu

181/61 211/71  
TAT GAA GTG AAA ATG ACA AAG GAA GTA TTG AAT AGA AAA CCA GGA AAA CCT TTC CCA AAA  
tyr glu val lys met thr lys glu val leu asn arg lys pro gly lys pro phe pro lys

241/81 271/91  
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lys thr glu ile pro ile pro asp arg ala lys leu phe trp gln his leu arg his glu

301/101 331/111  
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lys lys gln thr asp phe ile leu glu asp tyr val phe asp glu lys asp thr val tyr

361/121 391/131  
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ser val cys arg leu asn thr val thr ser lys met leu val ser glu lys val val lys

421/141 451/151  
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481/161 511/171  
CTT ACC TAT CGT AAA AAA TTT CAC CTG AAC TTT AGT CGA GAA AAT CCG GAA AAA GAC GAA  
leu thr tyr arg lys lys phe his leu asn phe ser arg glu asn pro glu lys asp glu

541/181 571/191  
GAA GCG AAT CGG AGT TAC AAA TTC CTG AAG AAT GTT ATG ACC CAG AAA GTT CGC TAC GCG  
glu ala asn arg ser tyr lys phe leu lys asn val met thr gln lys val arg tyr ala

601/201 631/211  
CCT TTT GTG AAC GAG GAG ATT AAA GTA CAA TTC GCG AAA AAT TTT GTG TAC GAT AAT AAT  
pro phe val asn glu glu ile lys val gin phe ala lys asn phe val tyr asp asn asn

561/221 691/231  
TCA ATT CTG CGA GTT COT GAA TCG TTT CAC GAT CCA AAC AGA TTC GAA CAA TCA TTA GAA  
ser ile leu arg val pro glu ser phe his asp pro asn arg phe glu gln ser leu glu

21/241 751/251

GTA GCA CCA ATC GAA GCA TGG TTT GGA ATT ATT GGA ATC AAA GAA TTG TTC GAT	val ala pro arg ile glu ala trp phe gly ile tyr ile gly ile lys glu leu phe asp
731/261	811/271
GGT GAA CCT GTG CTC AAT TTT GCA ATT GTC GAT AAA CTA TTC TAC AAT GCA CCG AAA ATG	gly glu pro val leu asn phe ala ile val asp lys leu phe tyr asn ala pro lys met
841/281	871/291
TCT CTT CTG GAT TAT CTT CTC CTA ATT GTC GAC CCC CAG TCG TGT AAC GAT GAT GTA CGA	ser leu leu asp tyr leu leu leu ile val asp pro gin ser cys asn asp asp val arg
901/301	931/311
AAA GAT CTT AAA ACA AAA CTG ATG GCG GGA AAA ATG ACA ATC AGA CAA GCC GCG CGG CCA	lys asp leu lys thr lys leu met ala gly lys met thr ile arg gin ala ala arg pro
961/321	991/331
AGA ATT CGA CAA TTA TTG GAA AAT TTG AAG CTG AAA TGC GCA GAA GTT TGG GAT AAC GAA	arg ile arg gin leu leu glu asn leu lys leu lys cys ala glu val trp asp asn glu
1021/341	1051/351
ATG TCG AGA TTG ACA GAA CGA CAT CTG ACA TTT CTA GAT TTG TGC GAG GAA AAC TCT CTT	met ser arg leu thr glu arg his leu thr phe leu asp leu cys glu glu asn ser leu
1081/361	1111/371
GTT TAT AAA GTC ACT GGT AAA TCG GAC AGA GGA AGA AAT GCA AAA AAG TAC GAT ACT ACA	val tyr lys val thr gly lys ser asp arg gly arg asn ala lys lys tyr asp thr thr
1141/381	1171/391
TTG TTC AAA ATC TAT GAG GAA AAC AAA AAG TTC ATT GAG TTT CCC CAC CTA CCA CTA GTC	leu phe lys ile tyr glu glu asn lys lys phe ile glu phe pro his leu pro leu val
1201/401	1231/411
AAA GTT AAA AGT GGA GCA AAA GAA TAC GCT GTA CCA ATG GAA CAT CTT GAA GTT CAT GAG	lys val lys ser gly ala lys glu tyr ala val pro met glu his leu glu val his glu
1261/421	1291/431
AAG CCA CAA AGA TAC AAG AAT CGA ATT GAT CTG GTG ATG CAA GAC AAG TTT CTA AAG CGA	lys pro gin arg tyr lys asn arg ile asp leu val met gin asp lys phe leu lys arg
1321/441	1351/451
GCT ACA CGA AAA CCT CAC GAC TAC AAA GAA AAT ACC CTA AAA ATG CTG AAA GAA TTG GAT	ala thr arg lys pro his asp tyr lys glu asn thr leu lys met leu lys glu leu asp
1381/461	1411/471
TTC TCT TCT GAA GAG CTA AAT TTT GTT GAA AGA TTT GGA TTA TGC TCC AAA CTT CAG ATG	phe ser ser glu glu leu asn phe val glu arg phe gly leu cys ser lys leu gin met
1441/481	1471/491
ATC GAA TGT CCA GGA AAG GTT TTG AAA GAG CCA ATG CTT GTG AAT AGT GTA AAT GAA CAA	ile glu cys pro gly lys val leu lys glu pro met leu val asn ser val asn glu gin
1501/501	1531/511
ATT AAA ATG ACA CCA GTG ATT CGT GGA TTT CAA GAA AAA CAA TTG AAT GTG GTT CCC GAA	ile lys met thr pro val ile arg gly phe gin glu lys gin leu asn val val pro glu

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lys glu leu cys cys ala val phe val val asn glu thr ala gly asn pro cys leu glu

AAC GAA ACA GCG GCA AAT CCA TGC TTA GAA  
 asn glu thr ala gly asn pro cys leu glu

1851/351  
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glu asn asp val val lys phe tyr thr glu leu ile gly gly cys lys phe arg gly ile

CTA ATT GGT GGT TGC AAG TTC CGT GGA ATA  
leu ile gly gly cys lys phe arg gly ile

CGA ATT GGT GCC AAT GAA AAC AGA GGA GCG CAA TCT ATT ATG TAC GAC GCG ACG AAA AAT  
arg ile gly ala asn glu asn arg gly ala gln ser ile met tyr asp ala thr lys asn

CRA TCT ATT ATG TAC GAC GCG ACG AAA AAT  
gin ser ile met tyr asp ala thr lys asn

GAA TAT GCC TTC TAC AAA AAT TGT ACA CTA AAT ACC GGA ATC GGT AGA TTT GAA ATA GCC  
glu tyr ala phe tyr lys asn cys thr leu asn thr gly ile gly arg phe glu ile ala

AAT ACC GGA ATC GGT AGA TTT GAA ATA GCC  
asn thr gly ile gly arg phe glu ile ala

GCA ACA GAA GCG AAG AAT ATG TTT GAA CGT CTT CCC GAT AAA GAA CAA AAA GTC TTA ATG  
ala thr glu ala lys asn met phe glu arg leu pro asp lys glu gin lys val leu met

CTT CCC GAT AAA GAA CAA AAA GTC TTA ATG  
leu pro asp lys glu gln lys val leu met

19917031  
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phe ile ile ile ser lys arg gin leu asn ala tyr gly phe val lys his tyr cys asp

GCT TAC GGT TTT GTG AAA CAT TAT TGC GAT  
ala tyr gly phe val lys his tyr cys asp

CAC ACC ATC GGT GTA GCT AAT CAG CAT ATT ACT TCT GAA ACA GTC ACA AAA GCT TTG GCA  
his thr ile gly val ala asn gin his ile thr ser glu thr val thr lys ala leu ala

ACT TCT GAA ACA GTC ACA AAA GCT TTG GCA  
thr ser glu thr val thr lys ala leu ala

2011/8/1  
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ser leu arg his glu lys gly ser lys arg ile phe tyr gln ile ala leu lys ile asn

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ile phe tyr gln ile ala leu lys ile asn

GCG AAA TTA GGA GGT ATT AAC CAG GAG CTT GAC TGG TCA GAA ATT GCA GAA ATA TCA CCA  
ala lys leu gly gly ile asn gln glu leu asp trp ser glu ile ala glu ile ser pro

GAC TGG TCA GAA ATT GCA GAA ATA TCA CCA  
asp trp ser glu ile ala glu ile ser pro

21517-21521

SPA GAA AAA GAA AGA CGG AAA ACA ATG CCA TTA ACT ATG TAT GTT CGA ATT GAT GTA ACT  
glu glu lys glu arg arg lys thr met pro leu thr met tyr val gly ile asp val thr

TTA ACT ATG TAT GTT GGA ATT GAT GTA ACT  
Leu thr met tyr val gly ile asp val thr

21917751  
CAT CCA ACC TCC TAC AGT GGA ATT GAT TAT TCT ATA GCG GCT GTA GTA GCG AGT ATC AAT  
his pro thr ser tyr ser gly ile asp tyr ser ile ala ala val val ala ser ile asn

CTT ATA GCG GCT GTA GTA GCG AGT ATC AAT  
ser ile ala ala val val ala ser ile asn

CCA GGT GGA ACT ATC TAT CGA AAT ATG ATT GTG ACT CAA GAA GAA TGT CGT CCC GGT GAG  
pro gly gly thr ile tyr arg asn met ile val thr gln glu glu cys arg pro gly glu

GTG ACT CAA GAA GAA TGT CGT CCC GGT GAG  
val thr gln glu glu cys arg pro gly glu

2511/771  
CCT GCA GTG GCT CAT GGA CGG GAA AGA ACA GAT ATT TTG GAA GCA AAG TTC GTG AAA TTG  
arg ala val ala his gly arg glu arg thr asp ile leu glu ala lys phe val lys leu

GAT ATT TTG GAA GCA AAG TTC GTG AAA TTG  
asp ile leu glu ala lys phe val lys leu

25717791  
TTC AGA GAA TTC GCA GAA AAC AAC GAC AAT CGA GCA CCA GCG CAT ATT GTA GTC TAT CGA  
Leu arg glu phe ala glu asn asn asp asn arg ala pro ala his ile val val tyr arg

CGA GCA CCA GCG CAT ATT GTA GTC TAT CGA  
arg ala pro ala his ile val val tyr arg

Parameter	Value	Unit
Initial concentration	1.0	g/L
Initial pH	7.0	
Temperature	25	°C
Time	0-120	min
Agitation speed	150	rpm
Agitation time	120	min
Agitation distance	10	cm
Agitation volume	100	ml
Agitation frequency	1	Hz
Agitation amplitude	1	mm
Agitation phase	0	rad
Agitation direction	0	deg
Agitation mode	0	deg
Agitation type	0	deg
Agitation class	0	deg
Agitation order	0	deg
Agitation level	0	deg
Agitation rank	0	deg
Agitation group	0	deg
Agitation category	0	deg
Agitation family	0	deg
Agitation series	0	deg
Agitation set	0	deg
Agitation subset	0	deg
Agitation superset	0	deg
Agitation disjoint	0	deg
Agitation overlap	0	deg
Agitation intersection	0	deg
Agitation union	0	deg
Agitation difference	0	deg
Agitation symmetric difference	0	deg
Agitation complement	0	deg
Agitation closure	0	deg
Agitation interior	0	deg
Agitation boundary	0	deg
Agitation exterior	0	deg
Agitation interior point	0	deg
Agitation boundary point	0	deg
Agitation exterior point	0	deg
Agitation interior line	0	deg
Agitation boundary line	0	deg
Agitation exterior line	0	deg
Agitation interior surface	0	deg
Agitation boundary surface	0	deg
Agitation exterior surface	0	deg
Agitation interior volume	0	deg
Agitation boundary volume	0	deg
Agitation exterior volume	0	deg
Agitation interior area	0	deg
Agitation boundary area	0	deg
Agitation exterior area	0	deg
Agitation interior length	0	deg
Agitation boundary length	0	deg
Agitation exterior length	0	deg
Agitation interior width	0	deg
Agitation boundary width	0	deg
Agitation exterior width	0	deg
Agitation interior height	0	deg
Agitation boundary height	0	deg
Agitation exterior height	0	deg
Agitation interior depth	0	deg
Agitation boundary depth	0	deg
Agitation exterior depth	0	deg
Agitation interior radius	0	deg
Agitation boundary radius	0	deg
Agitation exterior radius	0	deg
Agitation interior diameter	0	deg
Agitation boundary diameter	0	deg
Agitation exterior diameter	0	deg
Agitation interior circumference	0	deg
Agitation boundary circumference	0	deg
Agitation exterior circumference	0	deg
Agitation interior perimeter	0	deg
Agitation boundary perimeter	0	deg
Agitation exterior perimeter	0	deg
Agitation interior area	0	deg
Agitation boundary area	0	deg
Agitation exterior area	0	deg
Agitation interior volume	0	deg
Agitation boundary volume	0	deg
Agitation exterior volume	0	deg
Agitation interior length	0	deg
Agitation boundary length	0	deg
Agitation exterior length	0	deg
Agitation interior width	0	deg
Agitation boundary width	0	deg
Agitation exterior width	0	deg
Agitation interior height	0	deg
Agitation boundary height	0	deg
Agitation exterior height	0	deg
Agitation interior depth	0	deg
Agitation boundary depth	0	deg
Agitation exterior depth	0	deg
Agitation interior radius	0	deg
Agitation boundary radius	0	deg
Agitation exterior radius	0	deg
Agitation interior diameter	0	deg
Agitation boundary diameter	0	deg
Agitation exterior diameter	0	deg
Agitation interior circumference	0	deg
Agitation boundary circumference	0	deg
Agitation exterior circumference	0	deg
Agitation interior perimeter	0	deg
Agitation boundary perimeter	0	deg
Agitation exterior perimeter	0	deg
Agitation interior area	0	deg
Agitation boundary area	0	deg
Agitation exterior area	0	deg
Agitation interior volume	0	deg
Agitation boundary volume	0	deg
Agitation exterior volume	0	deg
Agitation interior length	0	deg
Agitation boundary length	0	deg
Agitation exterior length	0	deg
Agitation interior width	0	deg
Agitation boundary width	0	deg
Agitation exterior width	0	deg
Agitation interior height	0	deg
Agitation boundary height	0	deg
Agitation exterior height	0	deg
Agitation interior depth	0	deg
Agitation boundary depth	0	deg
Agitation exterior depth	0	deg
Agitation interior radius	0	deg
Agitation boundary radius	0	deg
Agitation exterior radius	0	deg
Agitation interior diameter	0	deg
Agitation boundary diameter	0	deg
Agitation exterior diameter	0	deg
Agitation interior circumference	0	deg
Agitation boundary circumference	0	deg
Agitation exterior circumference		



2401/801 2431/811  
 GAC GGA GTT AGC GAT TCG GAG ATG CTA CGT GTT AGT CAT GAT GAG CTT CGA TCT TTA AAA  
 asp gly val ser asp ser glu met leu arg val ser his asp glu leu arg ser leu lys

2461/821 2491/831  
 AGC GAA GTA AAA CAA TTC ATG TCG GAA CGG GAT GGA GAA GAT CCA GAG CCG AAG TAC ACG  
 ser glu val lys gln phe met ser glu arg asp gly glu asp pro glu pro lys tyr thr  
 2521/841 2551/851  
 TTC ATT GTG ATT CAG AAA AGA CAC AAT ACA CGA TTG CTT CGA AGA ATG GAA AAA GAT AAG  
 phe ile val ile gln lys arg his asn thr arg leu leu arg arg met glu lys asp lys

2581/861 2611/871  
 CCA GTG GTC AAT AAA GAT CTT ACT CCT GCT GAA ACA GAT GTC GCT GTT GCT GCT GTT AAA  
 pro val val asn lys asp leu thr pro ala glu thr asp val ala val ala val lys

2641/881 2671/891  
 CAA TGG GAG GAG GAT ATG AAA GAA AGC AAA GAA ACT GGA ATT GTG AAC CCA TCA TCC GGA  
 gln trp glu glu asp met lys glu ser lys glu thr gly ile val asn pro ser ser gly

2701/901 2731/911  
 ACA ACT GTG GAT AAA CTT ATC GTT TCG AAA TAC AAA TTC GAT TTT TTC TTG GCA TCT CAT  
 thr thr val asp lys leu ile val ser lys tyr lys phe asp phe phe leu ala ser his

2761/921 2791/931  
 CAT GGT GTC CTT GGT ACA TCT CGT CCA GGA CAT TAC ACT GTT ATG TAT GAC GAT AAA GGA  
 his gly val leu gly thr ser arg pro gly his tyr thr val met tyr asp asp lys gly

2821/941 2851/951  
 ATG AGC CAA GAT GAA GTC TAT AAA ATG ACC TAC GGA CTT GCT TTT CTC TCT GCT AGA TGT  
 met ser gln asp glu val tyr lys met thr tyr gly leu ala phe leu ser ala arg cys

2881/961 2911/971  
 CGA AAA CCC ATC TCG TTG CCT GTT CCG GTT CAT TAT GCT CAT TTA TCA TGT GAA AAA GCG  
 arg lys pro ile ser leu pro val pro val his tyr ala his leu ser cys glu lys ala

2941/981 2971/991  
 AAA GAG CTT TAT CGA ACT TAC AAG GAA CAT TAC ATC GGT GAC TAT GCA CAG CCA CGG ACT  
 lys glu leu tyr arg thr tyr lys glu his tyr ile gly asp tyr ala gln pro arg thr

3001/1001 3031/1011  
 CGA CAC GAA ATG GAA CAT TTT CTC CAA ACT AAC GTG AAG TAC CCT GGA ATG TCG TTC GCA  
 arg his glu met glu his phe leu gln thr asn val lys tyr pro gly met ser phe ala

3061/1021 3091/1031  
 TAA CAT TTT GCA AAA GTG TCG CCC GTT TCA ATC AAA TTT TTC AAT TGT AGA TAT TGT ACT  
 OCH (SEQ ID NO: 3)

3121/1041 3151/1051  
 TAC TTT TTT TTA AAG CCC GGT TTC AAA AAT TCA TTC CAT GAC TAA CGT TTT CAT AAA TTA

3181/1061  
 CTT GAA ATT TAA AAA AAA AAA AAA AAA (SEQ ID NO: 2)

Figure 7

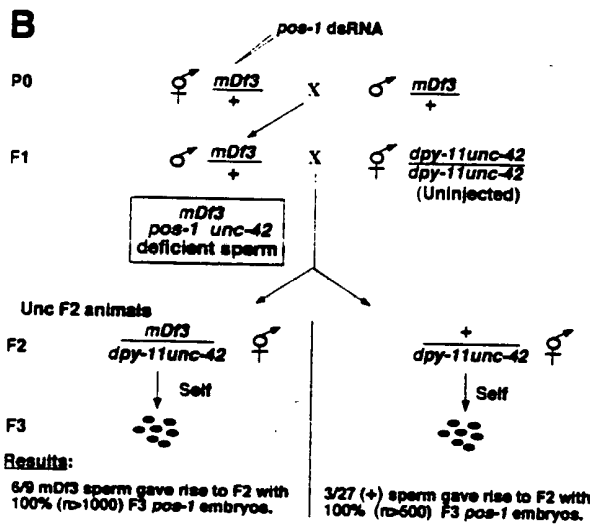
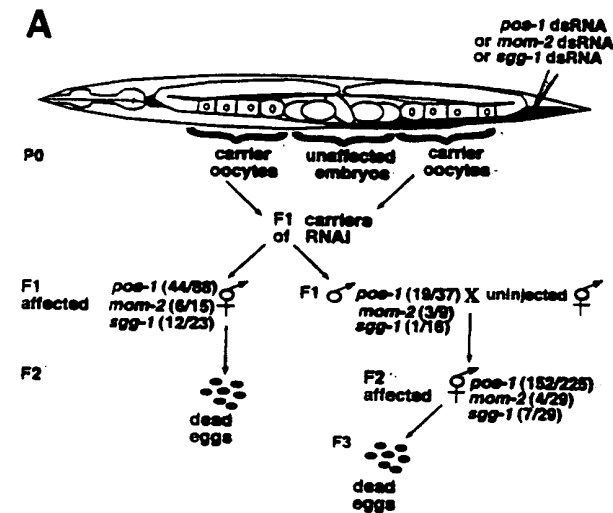


Figure 8

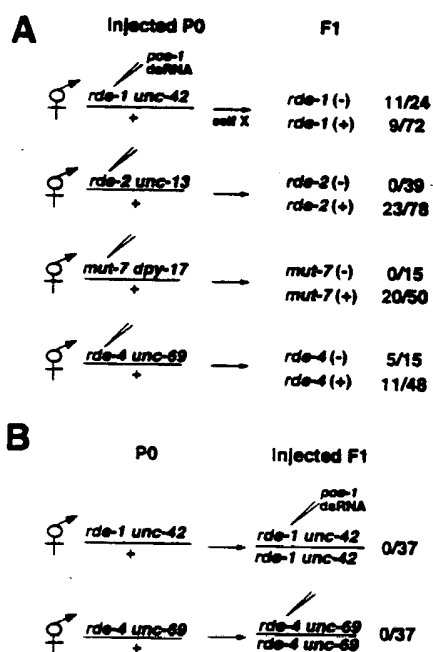
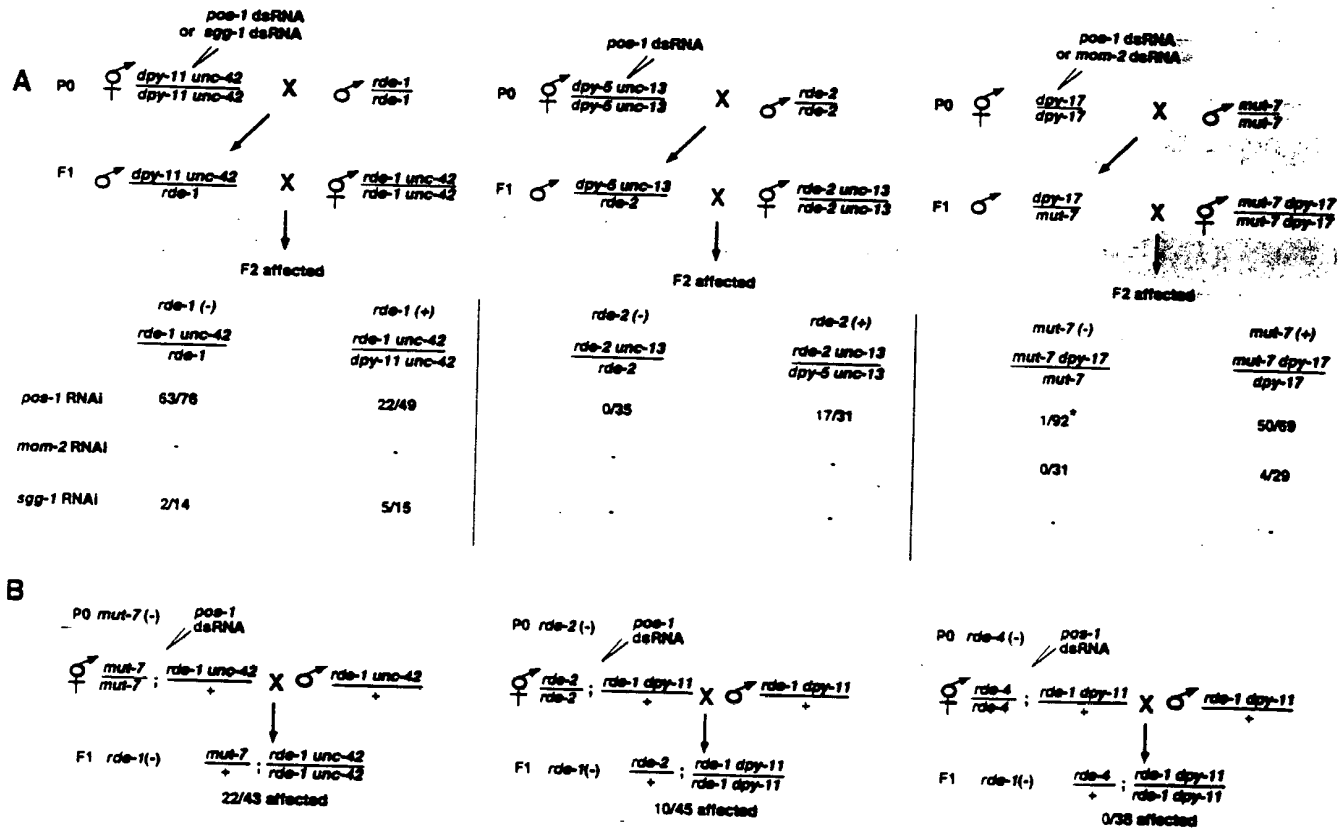


Figure 9



10998999-101000

10 20 30 40 50 60  
ATGGATTTAACCAAACCTGTTTGAAGCGTTTTCGGTGGATCAGATGTTCTCTATGAAG  
M D L T K L T F E S V F G G S D V P M K

70 80 90 100 110 120  
CCTTCCCAGATCGGAGGATAACAAAACGCCAAGAAACAGAACAGATTGAGATGTTTCTG  
P S R S E D N K T P R N R T D L E M F L

130 140 150 160 170 180  
AAGAAAACCTCCCTCATGGTACTAGAAGAGGCTGCTAAGGCTGTCTATCAAAGACGCCA  
K K T P L M V L E E A A K A V Y Q K T P

190 200 210 220 230 240  
ACTTGGGGCACTGTGGAACCTTCTGAAAGGCTTCGAGATGACGTTGATTCTGAATGAAATT  
T W G T V E L P E G F E M T L I L N E I

250 260 270 280 290 300  
ACTGTAAAAGGCCAGGCAACAAGCAAGAAAGCTGCGAGACAAAAGGCTGCTGTTGAATAT  
T V K G Q A T S K K A A R Q K A A V E Y

310 320 330 340 350 360  
TTACGCAAGGTTGTGAGAAAGGAAAGCACGAAATCTTTTTCATTCTCTGGAACAACCAAA  
L R K V V E K G K H E I F F I P G T T K

370 380 390 400 410 420  
GAAGAAGCTCTTTTGAATATTGATCAAATATCGGATAAGGCTGAGGAATTGAAACGATCA  
E E A L S N I D Q I S D K A E E L K R S

430 440 450 460 470 480  
ACTTCAGATGCTGTTTCAAGGATAACGATAACGATGATTTCGATTCTCTACAAGTCTGAATTT  
T S D A V Q D N D N D D S I P T S A E F

490 500 510 520 530 540  
CCACCTGGTATTTGCGCAACCGAGAATTGGGTGCGGAAAGTTGCAGGAAAAATCTCAAAA  
P P G I S P T E N W V G K L Q E K S Q K

550 560 570 580 590 600  
AGCAAGCTGCAAGCCCCAATCTATGAAGATTCCAAGATGAGAGAACCGAGCGTTTCTTG  
S K L Q A P I Y E D S K N E R T E R F L

610 620 630 640 650 660  
GTTATATGCACGATGTGCAATCAAAAAACCAGAGGAATCAGAAGTAAGAAGAAGGACGCA  
V I C T M C N Q K T R G I R S K K K D A

670 680 690 700 710 720  
AAGAATCTTGCAGCATGGTTGATGTGGAAGCGTTGGAAGACGGTATCGAATCTCTGGAA  
K N L A A W L M W K A L E D G I E S L E

730 740 750 760 770 780  
TCATATGATATGGTTGATGTGATTGAAAATTTGGAAGAAGCTGAACATTTACTCGAAATT  
S Y D M V D V I E N L E E A E H L L E I

CONFIDENTIAL

**TTATAAAAAAAAAAAAAA** (SEQ ID NO:4)  
L \* K K K K K (SEQ ID NO:5)

[illegible]

CONSENSUS P---L-E---Q---Y---GP-H---F---V---G---G-G-SKK---AK---AA---AL---L (500 bp)  
 Y H F SKQ K  
 α1 β1 β2

